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1644



1600

P#18

RAW SEQUENCE LISTING

DATE: 10/30/2002

PATENT APPLICATION: US/09/627,896A

TIME: 12:57:43

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3 <110> APPLICANT: CO, MAN SUNG
4 VASQUEZ, MAXIMILIANO
5 CARRENO, BEATRIZ
6 CELNIKER, ABBIE CHERYL
7 COLLINS, MARY
8 GOLDMAN, SAMUEL
9 GRAY, GARY S.
10 KNIGHT, ANDREA
11 O'HARA, DENISE
12 RUP, BONITA
13 VELDMAN, GEERTRUIDA M.
15 <120> TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
16 OF TREATMENT THEREWITH
18 <130> FILE REFERENCE: 08702.0081-01000
20 <140> CURRENT APPLICATION NUMBER: 09/627,896A
21 <141> CURRENT FILING DATE: 2000-07-27
23 <160> NUMBER OF SEQ ID NOS: 24
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29 <212> TYPE: DNA
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33 <221> NAME/KEY: CDS
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35 <223> OTHER INFORMATION: Anti-B7-2 heavy chain
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40 1 5 10 15
42 gtg cac tcc cag gtc cag ctg cag cag tct ggg cct gag ctg gtg agg 96
43 Val His Ser Gln Val Gln Leu Gln Ser Gly Pro Glu Leu Val Arg
44 20 25 30
46 cct ggg gaa tca gtg aag att tcc tgc aag ggt tcc ggc tac aca ttc 144
47 Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe
48 35 40 45
50 act gat tat gct ata cag tgg gtg aag cag agt cat gca aag agt cta 192
51 Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu
52 50 55 60
54 gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac 240
55 Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn
56 65 70 75 80
58 cag aag ttt aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc 288

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63 Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile
64      100      105      110
66 tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa gga   384
67 Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly
68      115      120      125
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88      20      25      30
90 Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe
91      35      40      45
93 Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu
94      50      55      60
96 Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn
97 65      70      75      80
99 Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser
100      85      90      95
102 Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile
103      100      105      110
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106      115      120      125
108 Thr Ser Val Thr Val Ser Ser
109      130      135
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118 <221> NAME/KEY: CDS
119 <222> LOCATION: (1)..(396)
120 <223> OTHER INFORMATION: Anti-B7-2 light chain
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124 Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Trp Val Ser
125 1      5      10      15
127 ggt acc tgt ggg gac att gtg ctg tca cag tct cca tcc tcc ctg gct   96

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132 Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
133          35          40          45
135 ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag 192
136 Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
137          50          55          60
139 aaa cca ggg cag tct cct aaa ctg ctg atc tac tgg gca tcc act agg 240
140 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
141 65          70          75          80
143 gaa tct ggg gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat 288
144 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
145          85          90          95
147 ttc act ctc acc atc agc agt gtg cag gct gaa gac ctg gca gtt tat 336
148 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
149          100          105          110
151 tac tgc acg caa tct tat aat ctt tac acg ttc gga ggg ggg acc aag 384
152 Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys
153          115          120          125
155 ctg gaa ata aaa 396
156 Leu Glu Ile Lys
157 130
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162 <212> TYPE: PRT
163 <213> ORGANISM: Murine sp.
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Anti-B7-2 light chain
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173          20          25          30
175 Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
176          35          40          45
178 Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
179          50          55          60
181 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
182 65          70          75          80
184 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
185          85          90          95
187 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
188          100          105          110
190 Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys
191          115          120          125
193 Leu Glu Ile Lys
194 130
197 <210> SEQ ID NO: 5

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RAW SEQUENCE LISTING

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206 <220> FEATURE:
207 <221> NAME/KEY: CDS
208 <222> LOCATION: (1)..(405)
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213   1             5             10             15
215 gtg cac tcc cag gtc cag ctg gtg cag tct ggg gct gag gtg aag aag      96
216 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
217             20             25             30
219 cct ggg agc tca gtg aag gtg tcc tgc aaa gct tcc ggc tac aca ttc      144
220 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
221             35             40             45
223 act gat tat gct ata cag tgg gtg aga cag gct cct gga cag ggc ctc      192
224 Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
225             50             55             60
227 gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac      240
228 Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn
229             65             70             75             80
231 cag aag ttt aag ggc aag gcc aca atg act gta gac aag tcg acg agc      288
232 Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser
233             85             90             95
235 aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat acg gcc gtt      336
236 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
237             100            105            110
239 tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa ggt      384
240 Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly
241             115            120            125
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244 Thr Leu Val Thr Val Ser Ser
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267 Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
268          50          55          60
270 Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn
271 65          70          75          80
273 Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser
274          85          90          95
276 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
277          100          105          110
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295 <220> FEATURE:
296 <221> NAME/KEY: CDS
297 <222> LOCATION: (1)..(396)
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302 1          5          10          15
304 ggc acc tgt ggg gac att gtg ctg aca cag tct cca gat tcc ctg gct      96
305 Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala
306          20          25          30
308 gta agc tta gga gag agg gcc act att agc tgc aaa tcc agt cag agt      144
309 Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser
310          35          40          45
312 ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag      192
313 Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
314          50          55          60
316 aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca tcc act agg      240
317 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
318 65          70          75          80
320 gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct ggg aca gat      288
321 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
322          85          90          95
324 ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg gca gtt tat      336
325 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
326          100          105          110
328 tac tgc acg caa tct tat aat ctt tac acg ttc gga cag ggg acc aag      384
329 Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys
330          115          120          125

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VERIFICATION SUMMARY

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